



BB-1163 US DIV Correct Sequence Listing

SEQUENCE LISTING

<110> Allen, Stephen M.  
Hitz, William D.  
Kinney, Anthony J.

<120> Plant Sugar Transport Proteins

<130> BB1163USDIV

<140> 10/051,902

<141> 2002-01-17

<150> 60/083,044

<151> 1998-04-24

<160> 30

<170> Microsoft Office 97

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<211> 2824

<212> DNA

<213> Zea mays

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<223> n = a, c, g or t

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<223> n = a, c, g or t

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## BB-1163 US DIV Correct Sequence Listing

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&lt;223&gt; n = a, c, g or t

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ggggatcacg	aaccttggcc	gccgctgccc	gagtgggggc	gtagatttcc	ggcggccatg	240
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cctctgatcg	aaggcctcat	cgtcgccatg	ttcctcattt	ggcaacagt	catcacaaca	420
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tccaatctaa	ttgatttggg	tacactagcc	catgcttgc	tctccaccat	cagtgttatac	2160
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caagcggctg	caaaagccta	atttcttgg	tacctttgt	tgcaactatt	gcactgttaag	2520
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gttaaggaa	cgaacatctg	ctcatgctcc	tcaaacggta	aaaaagagtc	cctcaatggc	2640
aataggagt	cgttaagttg	tcaatgtcat	ttaccatatg	tttacctat	ttgtactgt	2700

BB-1163 US DIV Correct Sequence Listing  
ttataagtca agctattcaa cgctgggtgt tgctagaaat ctttagaaca aagatgataa 2760  
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aaaaa 2824

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<212> PRT  
<213> Zea mays

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<223> xaa = any amino acid

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Lys Lys Glu Phe Asn Leu Gln Ser Glu Pro Leu Ile Glu Gly Leu Ile  
35 40 45  
Val Ala Met Phe Leu Ile Gly Ala Thr Val Ile Thr Thr Ser Pro Gly  
50 55 60  
Pro Arg Ala Asp Cys Val Gly Arg Arg Pro Met Leu Val Ala Ser Ala

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 65                    70                    75                    80

val Leu Tyr Phe Val Ser Gly Leu Val Met Leu Trp Ala Pro Ile Val  
                   85                        90                        95  
 Tyr Ile Leu Leu Leu Ala Arg Leu Ile Asp Gly Phe Gly Ile Gly Leu  
                   100                        105                        110  
 Ala Val Thr Leu Val Pro Leu Tyr Ile Ser Glu Thr Ala Pro His Arg  
                   115                        120                        125  
 xaa Ser Trp Gly xaa Xaa Asn Thr Leu Pro Gln Phe Ile Gly Val Xaa  
                   130                        135                        140  
 Gly Gly Met Phe Leu Ser Tyr Cys Met Val Phe Gly Met Ser Leu Met  
                   145                        150                        155                        160  
 Pro Lys Pro Asp Trp Arg Leu Met Leu Gly Val Leu Ser Ile Pro Ser  
                   165                        170                        175  
 Leu Xaa Tyr Phe Gly Leu Thr Val Phe Tyr Leu Pro Glu Ser Pro Arg  
                   180                        185                        190  
 Trp Leu Val Ser Lys Gly Arg Met Ala Glu Ala Lys Arg Val Xaa Gln  
                   195                        200                        205  
 Arg Leu Arg Gly Arg Glu Asp Val Ser Xaa Glu Xaa Ala Leu Leu Val  
                   210                        215                        220  
 Glu Gly Leu Gly Val Gly Lys Asp Thr Arg Ile Xaa Glu Tyr Ile Ile  
                   225                        230                        235                        240  
 Gly Pro Ala Thr Glu Ala Ala Asp Asp Leu Val Thr Asp Gly Asp Lys  
                   245                        250                        255  
 Glu Gln Ile Thr Leu Tyr Gly Pro Glu Glu Gly Gln Ser Trp Ile Ala  
                   260                        265                        270  
 Arg Pro Ser Lys Gly Pro Ile Met Leu Gly Ser Val Leu Ser Leu Ala  
                   275                        280                        285  
 Ser Arg His Gly Ser Met Val Asn Gln Ser Val Pro Leu Met Asp Pro  
                   290                        295                        300  
 Ile Val Thr Leu Phe Gly Ser Val His Glu Asn Met Pro Gln Ala Gly  
                   305                        310                        315                        320  
 Gly Ser Met Arg Ser Thr Leu Phe Pro Asn Phe Gly Ser Met Phe Ser  
                   325                        330                        335  
 Val Thr Asp Gln His Ala Lys Asn Glu Gln Trp Asp Glu Glu Asn Leu  
                   340                        345                        350  
 His Arg Asp Asp Glu Glu Tyr Ala Ser Asp Gly Ala Gly Gly Asp Tyr  
                   355                        360                        365  
 Glu Asp Asn Leu His Ser Pro Leu Leu Ser Arg Gln Ala Thr Gly Ala  
                   370                        375                        380  
 Glu Gly Lys Asp Ile Val His His Gly His Arg Gly Ser Ala Leu Ser  
                   385                        390                        395                        400  
 Met Arg Arg Gln Ser Leu Leu Gly Glu Gly Gly Asp Gly Val Ser Ser

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405

410

415

Thr Asp Ile Gly Gly Gly Trp Gln Leu Ala Trp Lys Trp Ser Glu Lys  
 420 425 430

Glu Gly Glu Asn Gly Arg Lys Glu Gly Gly Phe Lys Arg Val Tyr Leu  
 435 440 445

His Gln Glu Gly Val Pro Gly Ser Arg Arg Gly Ser Ile Val Ser Leu  
 450 455 460

Pro Gly Gly Asp Val Leu Glu Gly Ser Glu Phe Val His Ala Ala  
 465 470 475 480

Ala Leu Val Ser Gln Ser Ala Leu Phe Ser Lys Gly Leu Ala Glu Pro  
 485 490 495

Arg Met Ser Asp Ala Ala Met Val His Pro Ser Glu Val Ala Ala Lys  
 500 505 510

Gly Ser Arg Trp Lys Asp Leu Phe Glu Pro Gly Val Arg Arg Ala Leu  
 515 520 525

Leu Val Gly Val Gly Ile Gln Ile Leu Gln Gln Phe Ala Gly Ile Asn  
 530 535 540

Gly Val Leu Tyr Tyr Thr Pro Gln Ile Leu Glu Gln Ala Gly Val Ala  
 545 550 555 560

Val Ile Leu Ser Lys Phe Gly Leu Ser Ser Ala Ser Ala Ser Ile Leu  
 565 570 575

Ile Ser Ser Leu Thr Thr Leu Leu Met Leu Pro Cys Ile Gly Phe Ala  
 580 585 590

Met Leu Leu Met Asp Leu Ser Gly Arg Arg Phe Leu Leu Leu Gly Thr  
 595 600 605

Ile Pro Ile Leu Ile Ala Ser Leu Val Ile Leu Val Val Ser Asn Leu  
 610 615 620

Ile Asp Leu Gly Thr Leu Ala His Ala Leu Leu Ser Thr Ile Ser Val  
 625 630 635 640

Ile Val Tyr Phe Cys Cys Phe Val Met Gly Phe Gly Pro Ile Pro Asn  
 645 650 655

Ile Leu Cys Ala Glu Ile Phe Pro Thr Arg Val Arg Gly Leu Cys Ile  
 660 665 670

Ala Ile Cys Ala Phe Thr Phe Trp Ile Gly Asp Ile Ile Val Thr Tyr  
 675 680 685

Ser Leu Pro Val Met Leu Asn Ala Ile Gly Leu Ala Gly Val Phe Ser  
 690 695 700

Ile Tyr Ala Val Val Cys Leu Ile Ser Phe Val Phe Val Phe Leu Lys  
 705 710 715 720

Val Pro Glu Thr Lys Gly Met Pro Leu Glu Val Ile Thr Glu Phe Phe  
 725 730 735

Ala Val Gly Ala Lys Gln Ala Ala Ala Lys Ala

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745

<210> 3  
<211> 443  
<212> DNA  
<213> Oryza sativa

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<223> n = a, c, g or t

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tccagattcc cagccgcctc tcttcttgtt agggatccg aaatctcggt ggacgagaga 180  
cttggtgttta atnattcgcc ggccatggcg ggcgccgtgc tggtcgccc cgcggcctcc 240  
atcggcaact tgctgcaggg ctggataat gcaaccattg caggtgcggg actgtacatc 300  
aagaaggaat tcaacttgca tagcgacccc cttatcgaag gtctgatcgt gccatgtcg 360  
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tggcgccca tgctnatcnc ttc 443

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<212> PRT  
<213> Oryza sativa

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<223> Xaa = any amino acid

<220>  
<221> UNSURE  
<222> (130)  
<223> Xaa = any amino acid

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Glu Glu Leu Thr Pro Pro Pro Ser Ala Leu Asp Ser Leu Leu Gln Ile  
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Ser Pro Lys Ser Phe Pro Ile Trp Arg Glu Phe Pro Ile Tyr Leu Pro  
20 25 30  
His Leu Gly Val Pro Thr Ser Pro Ser Arg Phe Pro Ala Ala Ser Leu  
35 40 45  
Leu Val Arg Gly Ser Glu Ile Ser Val Asp Glu Arg Leu Gly Gly Asn

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50 55 60

xaa Ser Pro Ala Met Ala Gly Ala Val Leu Val Ala Ile Ala Ala Ser  
65 70 75 80  
Ile Gly Asn Leu Leu Gln Gly Trp Asp Asn Ala Thr Ile Ala Gly Ala  
85 90 95  
Val Leu Tyr Ile Lys Lys Glu Phe Asn Leu His Ser Asp Pro Leu Ile  
100 105 110  
Glu Gly Leu Ile Val Ala Met Ser Leu Ile Gly Ala Thr Ile Ile Thr  
115 120 125  
Thr xaa Ser  
130

<210> 5  
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<212> DNA  
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tattccaaac attctctgtg cagagattt cccgaccacc gttcgtggca tctgcatacg 180  
catctgtgcc ctaacattct ggatcggtga tatcattgtg acatacaccc tccccgtgat 240  
gctcaacgcc attggactcg ctggagtggtt tggaatctac gcagtggct gcatactggc 300  
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cgagttcttc tctgtcggag caaagcaggc caaggaggac tagttgctcg gatcaagtga 420  
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gatggatgct ttgttaaaga atcttggaaag agatcaaaat gcagtgagcc taaagagatg 540  
atttggctgt acatcatgag gctgaatcct gtcgttagact ggattttgga gcttaggata 600  
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gttttcttct ctcgggtgtg agttctgaat attagcatag ccgagacta gttctgaatt 780  
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<210> 6  
<211> 131  
<212> PRT  
<213> Oryza sativa

<400> 6  
Val Leu Thr Leu Ile Leu Val Asn Ile Leu Asp Val Gly Thr Met Val  
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His Ala Ser Leu Ser Thr Val Ser Val Ile Leu Tyr Phe Cys Phe Phe  
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Val Met Gly Phe Gly Pro Ile Pro Asn Ile Leu Cys Ala Glu Ile Phe  
35 40 45  
Pro Thr Thr Val Arg Gly Ile Cys Ile Ala Ile Cys Ala Leu Thr Phe  
50 55 60  
Trp Ile Gly Asp Ile Ile Val Thr Tyr Thr Leu Pro Val Met Leu Asn  
65 70 75 80  
Ala Ile Gly Leu Ala Gly Val Phe Gly Ile Tyr Ala Val Val Cys Ile  
85 90 95

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Leu Ala Phe Leu Phe Val Phe Met Lys Val Pro Glu Thr Lys Gly Met  
100 105 110

Pro Leu Glu Val Ile Thr Glu Phe Phe Ser Val Gly Ala Lys Gln Ala  
115 120 125

Lys Glu Asp  
130

<210> 7  
<211> 2601  
<212> DNA  
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tcccaactaa	ctagcagttc	cttgcgtgt	ctccttcttc	accatatcgc	agtaatgaaa	180
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cttgatggat	ttgggattgg	cctgctgt	actcttgc	cggtctat	atctgaaacg	540
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ctcgggattt	ggggtgatac	atctatcgaa	gagtacataa	ttggccctgc	tgacgatgt	900
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gatgataatt	tgcacagtcc	tttatctca	cgccaaacaa	caagccttga	aaaagactta	1320
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gaatttgc	aggctgctgc	cttggtaagc	caaccgc	tttactccaa	ggagcttatt	1620
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ccaaacatcc	tttgc	gatttccc	actagggt	gtggcctct	cattgctatc	2160
tgtgcattag	tgttctggat	tggagacatc	atcatcacat	actcgctg	tgtgatgctc	2220
ggctctttag	gacttgg	tgtattcg	attacgcag	ttgtttgtt	catctcg	2280
atatttgtgt	tttgaaggt	tccagaaaca	aaggcatgc	cccttgaagt	catctctgaa	2340
ttcttttctg	ttggagcaaa	gcaggctgt	tctgccaaga	atgagtgaca	caacacaagt	2400
ccgttatata	ctctgtact	ttagttgtt	aagccatcat	ctctcg	tacagattt	2460
gctttcata	agtttattt	gaggaagata	ttttgaaaca	tatgggttt	ttttctt	2520
ataaaaaataa	aacccttccc	ttttgggt	ggaaaagaa	aaaaaaaaaa	aaaaaaaaaa	2580
aaaaaaaaaa	aaaaaaaaaa	a				2601

<210> 8  
<211> 737  
<212> PRT

## BB-1163 US DIV Correct Sequence Listing

&lt;213&gt; Glycine max

<400> 8  
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 Leu Gln Gly Trp Asp Asn Ala Thr Ile Ala Gly Ala Asn Gly Tyr Ile  
 20 25 30  
 Lys Lys Asp Leu Ala Leu Gly Thr Thr Met Glu Arg Leu Val Val Gly  
 35 40 45  
 Met Ser Leu Ile Gly Ala Thr Val Ile Thr Thr Cys Ser Gly Pro Ile  
 50 55 60  
 Ala Asp Trp Leu Gly Arg Arg Pro Met Met Ile Ile Ser Ser Val Leu  
 65 70 75 80  
 Tyr Phe Leu Gly Gly Leu Val Met Leu Trp Ser Pro Asn Val Tyr Val  
 85 90 95  
 Leu Cys Leu Ala Arg Leu Leu Asp Gly Phe Gly Ile Gly Leu Ala Val  
 100 105 110  
 Thr Leu Val Pro Val Tyr Ile Ser Glu Thr Ala Pro Ser Glu Ile Arg  
 115 120 125  
 Gly Ser Leu Asn Thr Leu Pro Gln Phe Ser Gly Ser Gly Gly Met Phe  
 130 135 140  
 Leu Ser Tyr Cys Met Val Phe Gly Met Ser Leu Ser Pro Ala Pro Ser  
 145 150 155 160  
 Trp Arg Leu Met Leu Gly Val Leu Ser Ile Pro Ser Leu Leu Tyr Phe  
 165 170 175  
 Ala Leu Thr Ile Phe Phe Leu Pro Glu Ser Pro Arg Trp Leu Val Ser  
 180 185 190  
 Lys Gly Arg Met Leu Glu Ala Lys Lys Val Leu Gln Arg Leu Arg Gly  
 195 200 205  
 Arg Glu Asp Val Ser Gly Glu Met Ala Leu Leu Val Glu Gly Leu Gly  
 210 215 220  
 Ile Gly Gly Asp Thr Ser Ile Glu Glu Tyr Ile Ile Gly Pro Ala Asp  
 225 230 235 240  
 Asp Val Ala Asp Gly His Glu His Ala Thr Glu Lys Asp Lys Ile Arg  
 245 250 255  
 Leu Tyr Gly Ser Gln Ala Gly Leu Ser Trp Leu Ser Lys Pro Val Thr  
 260 265 270  
 Gly Gln Ser Ser Ile Gly Leu Ala Ser His His Gly Ser Ile Ile Asn  
 275 280 285  
 Gln Ser Met Pro Leu Met Asp Pro Leu Val Thr Leu Phe Gly Ser Ile  
 290 295 300  
 His Glu Lys Leu Pro Glu Thr Gly Ala Arg Gly Ser Met Arg Ser Thr  
 305 310 315 320

BB-1163 US DIV Correct Sequence Listing

Leu Phe Pro Asn Phe Gly Ser Met Phe Ser Thr Ala Glu Pro His Ala  
325 330 335

Lys Ile Glu Gln Trp Asp Glu Glu Ser Leu Gln Arg Glu Arg Glu Asp  
340 345 350

Tyr Met Ser Asp Ala Thr Arg Gly Asp Ser Asp Asp Asn Leu His Ser  
355 360 365

Pro Leu Ile Ser Arg Gln Thr Thr Ser Leu Glu Lys Asp Leu Pro Pro  
370 375 380

Pro Pro Ser His Gly Ser Ile Leu Gly Ser Met Arg Arg His Ser Ser  
385 390 395 400

Leu Met Gln Gly Ser Gly Glu Gln Gly Gly Ser Thr Gly Ile Gly Gly  
405 410 415

Gly Trp Gln Leu Ala Trp Lys Trp Thr Asp Lys Gly Glu Asp Gly Lys  
420 425 430

Gln Gln Gly Phe Lys Arg Ile Tyr Leu His Glu Glu Gly Val Ser  
435 440 445

Ala Ser Arg Arg Gly Ser Ile Val Ser Ile Pro Gly Glu Gly Glu Phe  
450 455 460

Val Gln Ala Ala Ala Leu Val Ser Gln Pro Ala Leu Tyr Ser Lys Glu  
465 470 475 480

Leu Ile Asp Gly His Pro Val Gly Pro Ala Met Val His Pro Ser Glu  
485 490 495

Thr Ala Ser Lys Gly Pro Ser Trp Lys Ala Leu Leu Glu Pro Gly Val  
500 505 510

Lys His Ala Leu Val Val Gly Val Gly Ile Gln Ile Leu Gln Gln Phe  
515 520 525

Ser Gly Ile Asn Gly Val Leu Tyr Tyr Thr Pro Gln Ile Leu Glu Glu  
530 535 540

Ala Gly Val Glu Val Leu Leu Ser Asp Ile Gly Ile Gly Ser Glu Ser  
545 550 555 560

Ala Ser Phe Leu Ile Ser Ala Phe Thr Thr Phe Leu Met Leu Pro Cys  
565 570 575

Ile Gly Val Ala Met Lys Leu Met Asp Val Ser Gly Arg Arg Gln Leu  
580 585 590

Leu Leu Thr Thr Ile Pro Val Leu Ile Val Ser Leu Ile Ile Leu Val  
595 600 605

Ile Gly Ser Leu Val Asn Phe Gly Asn Val Ala His Ala Ala Ile Ser  
610 615 620

Thr Val Cys Val Val Val Tyr Phe Cys Cys Phe Val Met Gly Tyr Gly  
625 630 635 640

Pro Ile Pro Asn Ile Leu Cys Ser Glu Ile Phe Pro Thr Arg Val Arg  
645 650 655

BB-1163 US DIV Correct Sequence Listing

Gly	Leu	Cys	Ile	Ala	Ile	Cys	Ala	Leu	Val	Phe	Trp	Ile	Gly	Asp	Ile
660						665						670			
Ile	Ile	Thr	Tyr	Ser	Leu	Pro	Val	Met	Leu	Gly	Ser	Leu	Gly	Leu	Gly
675					680					685					
Gly	Val	Phe	Ala	Ile	Tyr	Ala	Val	Val	Cys	Phe	Ile	Ser	Trp	Ile	Phe
690					695				700						
Val	Phe	Leu	Lys	Val	Pro	Glu	Thr	Lys	Gly	Met	Pro	Leu	Glu	Val	Ile
705				710				715				720			
Ser	Glu	Phe	Phe	Ser	Val	Gly	Ala	Lys	Gln	Ala	Ala	Ser	Ala	Lys	Asn
	725					730						735			

Glu

<210> 9  
<211> 1692  
<212> DNA  
<213> Glycine max

<400> 9  
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agtcctgggt tgcttagacct gttgctggac caaattctgt tggccttgc tcttagaaag 120  
gaagcatggc aaatccaagc agtctagtgg accctctagt gaccctcttt ggttagtgtac 180  
atgagaagct cccagaaaaca ggaagcaccc ttttccaca ctttgggagt atgttcagtg 240  
ttgggggaaa tcagccaagg aatgaagatt gggatgagga aagcctagcc agagagggtg 300  
atgattatgt ctctgatgct ggtgattctg atgacaattt gcagagtcca ttgatctcac 360  
gtcaaacaac gagtctggat aaggacatac ctcctcatgc ccatagtaac cttgcaagca 420  
tgaggcaagg tagtctttt catggaaatt caggagaacc cactggtagt actgggattg 480  
gtggtggttg gcagctagca tggaaatggt ctgaaagaga gggcccagat ggaaagaagg 540  
aaggtagctt caagagaata tatttacacc aagatggtg ttctggatct agacgtgggt 600  
ctgtggtttc actccctggc ggtgatttac caactgacag tgaggttgc caggctgctg 660  
ctctggtgag tcagcctgcc ctttataatg aggaccttat gcgtcaacgg ccagttggac 720  
cagctatgat tcatccctct gaaacaattt gaaaagggcc aagttggagt gatcttttg 780  
aacctgggtt gaagcatgca ttgattgtgg gggtgggaat gcaaattctt cagcagttct 840  
ctggataaaa tggggtcctc tactatacgc ctcaatttct tgagcaggca ggtgttggtt 900  
atcttcttc aaggcttaggc cttggttcta cttcttcattt ctttcttatt agtgcgggtga 960  
caaccttgtt gatgcttcct tgtatagccca ttgccccatgag gctcatggat atttcaggca 1020  
gaaggacttt gctgctcagt acaatccccg tcctaatagc agctcttctc atattagtcc 1080  
tgggaagtct tggatggattt ggttccactg caaatgcattt aatctcaacc attagtgtta 1140  
ttgtctattt ctgtttctt gtcatggat ttggaccaat tcctaatata ctttgtgcag 1200  
agatcttccc cactcgagtt cgtggctct gcattgctat ttgtgccctt accttttggaa 1260  
tctgtgatat cattgtcacc tacacactcc cagttatgct caattctgtt ggcctcgctg 1320  
gtgttttggg tatttatgct gtcgtgtgct tcatagcatg ggtgtttgtc tttttgaaag 1380  
ttccagaaaac caagggcatg ccactggaaag tgatcattga gttttcttctt gtcggagcaa 1440  
aacagttga cgatgccaag cacaactgac ccaaggacat gataaattca aagttttgac 1500  
gttaccttctt aattattttc aatctacggc ttgttggaaat tttccctctt tttaaaattt 1560  
tattttctat ttattctctc tttccgtgg gttgagattt agaaacaaga aactttgttt 1620  
ctgtaaagaa aaatgttcat tttctgggttca atttatggaa ctttatatac ttccctaaaaaa 1680  
aaaaaaaaaa aa 1692

<210> 10  
<211> 486  
<212> PRT  
<213> Glycine max

<400> 10  
Asp Pro Ser Arg Glu Lys Asp Gln Ile Lys Leu Tyr Gly Pro Glu Gln  
1 5 10 15

BB-1163 US DIV Correct Sequence Listing

Gly Gln Ser Trp Val Ala Arg Pro Val Ala Gly Pro Asn Ser Val Gly  
20 25 30

Leu Val Ser Arg Lys Gly Ser Met Ala Asn Pro Ser Ser Leu Val Asp  
35 40 45

Pro Leu Val Thr Leu Phe Gly Ser Val His Glu Lys Leu Pro Glu Thr  
50 55 60

Gly Ser Thr Leu Phe Pro His Phe Gly Ser Met Phe Ser Val Gly Gly  
65 70 75 80

Asn Gln Pro Arg Asn Glu Asp Trp Asp Glu Glu Ser Leu Ala Arg Glu  
85 90 95

Gly Asp Asp Tyr Val Ser Asp Ala Gly Asp Ser Asp Asp Asn Leu Gln  
100 105 110

Ser Pro Leu Ile Ser Arg Gln Thr Thr Ser Leu Asp Lys Asp Ile Pro  
115 120 125

Pro His Ala His Ser Asn Leu Ala Ser Met Arg Gln Gly Ser Leu Leu  
130 135 140

His Gly Asn Ser Gly Glu Pro Thr Gly Ser Thr Gly Ile Gly Gly Gly  
145 150 155 160

Trp Gln Leu Ala Trp Lys Trp Ser Glu Arg Glu Gly Pro Asp Gly Lys  
165 170 175

Lys Glu Gly Gly Phe Lys Arg Ile Tyr Leu His Gln Asp Gly Gly Ser  
180 185 190

Gly Ser Arg Arg Gly Ser Val Val Ser Leu Pro Gly Gly Asp Leu Pro  
195 200 205

Thr Asp Ser Glu Val Val Gln Ala Ala Ala Leu Val Ser Gln Pro Ala  
210 215 220

Leu Tyr Asn Glu Asp Leu Met Arg Gln Arg Pro Val Gly Pro Ala Met  
225 230 235 240

Ile His Pro Ser Glu Thr Ile Ala Lys Gly Pro Ser Trp Ser Asp Leu  
245 250 255

Phe Glu Pro Gly Val Lys His Ala Leu Ile Val Gly Val Gly Met Gln  
260 265 270

Ile Leu Gln Gln Phe Ser Gly Ile Asn Gly Val Leu Tyr Tyr Thr Pro  
275 280 285

Gln Ile Leu Glu Gln Ala Gly Val Gly Tyr Leu Leu Ser Ser Leu Gly  
290 295 300

Leu Gly Ser Thr Ser Ser Ser Phe Leu Ile Ser Ala Val Thr Thr Leu  
305 310 315 320

Leu Met Leu Pro Cys Ile Ala Ile Ala Met Arg Leu Met Asp Ile Ser  
325 330 335

Gly Arg Arg Thr Leu Leu Leu Ser Thr Ile Pro Val Leu Ile Ala Ala  
340 345 350

BB-1163 US DIV Correct Sequence Listing

Leu Leu Ile Leu Val Leu Gly Ser Leu Val Asp Leu Gly Ser Thr Ala  
355 360 365

Asn Ala Ser Ile Ser Thr Ile Ser Val Ile Val Tyr Phe Cys Phe Phe  
370 375 380

Val Met Gly Phe Gly Pro Ile Pro Asn Ile Leu Cys Ala Glu Ile Phe  
385 390 395 400

Pro Thr Arg Val Arg Gly Leu Cys Ile Ala Ile Cys Ala Leu Thr Phe  
405 410 415

Trp Ile Cys Asp Ile Ile Val Thr Tyr Thr Leu Pro Val Met Leu Asn  
420 425 430

Ser Val Gly Leu Ala Gly Val Phe Gly Ile Tyr Ala Val Val Cys Phe  
435 440 445

Ile Ala Trp Val Phe Val Phe Leu Lys Val Pro Glu Thr Lys Gly Met  
450 455 460

Pro Leu Glu Val Ile Ile Glu Phe Phe Ser Val Gly Ala Lys Gln Phe  
465 470 475 480

Asp Asp Ala Lys His Asn  
485

<210> 11  
<211> 510  
<212> DNA  
<213> Triticum aestivum

<220>  
<221> unsure  
<222> (421)  
<223> n = a, c, g or t

<220>  
<221> unsure  
<222> (434)  
<223> n = a, c, g or t

<220>  
<221> unsure  
<222> (441)  
<223> n = a, c, g or t

<220>  
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<222> (458)  
<223> n = a, c, g or t

<220>  
<221> unsure  
<222> (483)  
<223> n = a, c, g or t

<220>  
<221> unsure  
<222> (493)  
<223> n = a, c, g or t

<220>

BB-1163 US DIV Correct Sequence Listing

<221> unsure

<222> (498)

<223> n = a, c, g or t

<400> 11

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ctcggttctg	atctaccgca	ccacaccacc	acaccacacc	aggggcctgc	cgcttcttgg	120
gcttctccat	ctcatctcct	tggttgggtc	tctactagag	aggcgagct	gcagggatcc	180
ttggtgggaga	ggagggagaaga	agatgtcggg	tgctgcactg	gtcgcgattg	cggcttccat	240
tggcaatctg	ctgcagggtt	gggacaatgc	caccatcgct	ggtgctgttc	tgtacatcaa	300
gaaggaattc	cagctcgaaa	ataatccgac	tgtggagggg	ctcatcgtgg	catgtcctca	360
tcgggtgcaa	catcatcaca	cattctccgg	gccagtatca	aactgggttq	ccgggccccta	420
ngccatctcc	ttgnnttcaa	ntcccaaggg	ctaatacanc	aggcaccaat	gtcaatgtgc	480
gcnccggAAC	ctntcaangg	ttggaacgtt				510

<210> 12

<211> 117

<212> PRT

<213> Triticum aestivum

<400> 12

Gly	Gly	Ser	Arg	Gly	Ser	Glu	Gly	Gly	Val	Ala	Leu	Gly	Ser	Tyr	Leu
1				5					10				15		

Arg	Arg	Leu	Arg	Ser	Val	Leu	Ile	Tyr	Arg	Thr	Thr	Pro	Pro	His	His
							20		25				30		

Thr	Arg	Gly	Leu	Pro	Leu	Leu	Gly	Leu	Leu	His	Leu	Ile	Ser	Leu	Val
							35		40			45			

Gly	Ser	Leu	Leu	Glu	Arg	Arg	Ser	Cys	Arg	Asp	Pro	Trp	Trp	Arg	Gly
					50		55			60					

Gly	Lys	Lys	Met	Ser	Gly	Ala	Ala	Leu	Val	Ala	Ile	Ala	Ala	Ser	Ile
					65		70			75				80	

Gly	Asn	Leu	Leu	Gln	Gly	Trp	Asp	Asn	Ala	Thr	Ile	Ala	Gly	Ala	Val
					85			90			95				

Leu	Tyr	Ile	Lys	Lys	Glu	Phe	Gln	Leu	Glu	Asn	Asn	Pro	Thr	Val	Glu
					100			105				110			

Gly	Leu	Ile	val	Ala
			115	

<210> 13

<211> 1487

<212> DNA

<213> Triticum aestivum

<400> 13

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tcgcattggaa	atggtcggag	cgacaaggcg	aggatggcaa	gaaggaagga	ggcttcaaaa	120
gaatctactt	gcaccaagag	gggggtggccg	actcaagaag	gggctctgtt	gttcaacttc	180
ctgggtgggg	tgatgccacg	caagggggca	gtgggttat	acatgctgct	gctttggtaa	240
gccactcggc	tctttactcc	aaggatctta	tggaagagcg	tatggcggcc	ggtccagcca	300
tgattcatcc	attggaggca	gctcccaaag	gttcaatctg	gaaagatctg	tttgaacctg	360
gtgtgaggcg	tgcattgttc	gtcgggtttg	gaattcagat	gcttcagcag	tttgctggaa	420
taaatggagt	tctctactat	actcctcaaa	ttctggagca	agctggtgtg	gctgttcttc	480
tttccaatct	tggcctcagt	tcagcatcag	catccatctt	gatcagttct	ctcaccaccc	540
tactcatgct	cccaagcatt	ggtgttagcca	tgagacttat	ggatatatct	ggaagaaggt	600
ttctgctact	gggcacaatt	cccatcttga	tagcatccct	aattgttttgg	ggtgtggtca	660
atgttatcaa	cttgagtacg	gtgccccacg	ctgtgctctc	cacagttagc	gtcattgtct	720

## BB-1163 US DIV Correct Sequence Listing

acttctgctg	ctttgtcatg	ggctttggcc	cgatccccaa	cattctatgt	gcagagattt	780
tcccccaccag	agtccgtgg	gtctgcacatcg	ctatttgcgc	cctcacattc	tggatttgg	840
acattattgt	tacctacagc	ctgcctgtga	tgctgaatgc	tattggtcta	gcgggtgtct	900
ttggtatata	tgcagtcgtt	tgctgcattg	cctttgtgtt	cgtctaccta	aagggtcccag	960
agacaaaagg	catgcccctc	gaggtcatca	ccgagttctt	tgcgggtggg	gcgaagcaag	1020
cgcaggccac	cattgcctga	ttcatcatgg	agctttgttt	tcagttgca	cactgcggc	1080
tgcgctgaaa	attgcaaatt	ggacgggtcc	tcgtgaggaa	cggaaaaact	tttgagttgt	1140
aatgagaca	gctacccaaa	gagctcatca	cgaggaacgg	gaagctgtaa	aagtaggagg	1200
atctcatgcc	cccatttcat	cgtctattat	tgcttattag	tactgtactg	taatcgcat	1260
tagttgtgt	agggttgttc	aacttgctaa	tctgattctg	aactaccatg	ctgatgtccg	1320
aaataaagaa	aaagcatgtt	ttttttgtg	tcaacttgca	aactttctt	taaacattgt	1380
gcaatgtatt	gtaaatttct	ttatcaactt	ccctcgattc	agagagaagc	acttgtttgt	1440
aagtcatgaa	agattttct	cgacaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		1487

&lt;210&gt; 14

&lt;211&gt; 345

&lt;212&gt; PRT

&lt;213&gt; Triticum aestivum

&lt;400&gt; 14

Ser	Trp	Lys	Glu	Gly	Gly	Glu	Ala	Val	Ser	Ser	Thr	Gly	Ile	Gly	Gly
1				5				10						15	

Gly	Trp	Gln	Leu	Ala	Trp	Lys	Trp	Ser	Glu	Arg	Gln	Gly	Glu	Asp	Gly
						20		25				30			

Lys	Lys	Glu	Gly	Gly	Phe	Lys	Arg	Ile	Tyr	Leu	His	Gln	Glu	Gly	Val
						35		40				45			

Ala	Asp	Ser	Arg	Arg	Gly	Ser	Val	Val	Ser	Leu	Pro	Gly	Gly	Asp	
						50		55			60				

Ala	Thr	Gln	Gly	Gly	Ser	Gly	Phe	Ile	His	Ala	Ala	Ala	Leu	Val	Ser
						65		70			75		80		

His	Ser	Ala	Leu	Tyr	Ser	Lys	Asp	Leu	Met	Glu	Glu	Arg	Met	Ala	Ala
						85			90			95			

Gly	Pro	Ala	Met	Ile	His	Pro	Leu	Glu	Ala	Ala	Pro	Lys	Gly	Ser	Ile
						100		105				110			

Trp	Lys	Asp	Leu	Phe	Glu	Pro	Gly	Val	Arg	Arg	Ala	Leu	Phe	Val	Gly
						115		120				125			

Val	Gly	Ile	Gln	Met	Leu	Gln	Gln	Phe	Ala	Gly	Ile	Asn	Gly	Val	Leu
						130		135			140				

Tyr	Tyr	Thr	Pro	Gln	Ile	Leu	Glu	Gln	Ala	Gly	Val	Ala	Val	Leu	Leu
						145		150			155			160	

Ser	Asn	Leu	Gly	Leu	Ser	Ser	Ala	Ser	Ala	Ser	Ile	Leu	Ile	Ser	Ser
						165			170			175			

Leu	Thr	Thr	Leu	Leu	Met	Leu	Pro	Ser	Ile	Gly	Val	Ala	Met	Arg	Leu
						180			185			190			

Met	Asp	Ile	Ser	Gly	Arg	Arg	Phe	Leu	Leu	Leu	Gly	Thr	Ile	Pro	Ile
						195		200			205				

Leu	Ile	Ala	Ser	Leu	Ile	Val	Leu	Gly	Val	Val	Asn	Val	Ile	Asn	Leu
						210		215			220				

Ser	Thr	Val	Pro	His	Ala	Val	Leu	Ser	Thr	Val	Ser	Val	Ile	Val	Tyr

BB-1163 US DIV Correct Sequence Listing

225	230	235	240
Phe Cys Cys Phe Val Met Gly Phe Gly Pro Ile Pro Asn Ile Leu Cys			
245	250		255
Ala Glu Ile Phe Pro Thr Arg Val Arg Gly Val Cys Ile Ala Ile Cys			
260	265		270
Ala Leu Thr Phe Trp Ile Cys Asp Ile Ile Val Thr Tyr Ser Leu Pro			
275	280		285
Val Met Leu Asn Ala Ile Gly Leu Ala Gly Val Phe Gly Ile Tyr Ala			
290	295		300
Val Val Cys Cys Ile Ala Phe Val Phe Val Tyr Leu Lys Val Pro Glu			
305	310	315	320
Thr Lys Gly Met Pro Leu Glu Val Ile Thr Glu Phe Phe Ala Val Gly			
325	330		335
Ala Lys Gln Ala Gln Ala Thr Ile Ala			
340	345		

<210> 15  
<211> 1009  
<212> DNA  
<213> Triticum aestivum

<400> 15  
tgaacctgga gtgaagcatg cactgttcgt tggcatagga ttacagatcc tgcagcagtt 60  
tgcgggtatc aatggagtcc tctactacac acctcagata cttgagcaag caggtgtcgg 120  
gtttcttcta tcaaacattg gactaagctc ttcctcagca tctattctta ttagtgcctt 180  
gacaacctg ctgatgcttc ccagcattgg catcgccatg agactcatgg atatgtcagg 240  
aagaaggttt cttctccctt caacaatccc tgtcttgata gtagcgctag ctgtcttgg 300  
tttagtgaat gttctggatg tcggaaccat ggtgcacgct gcgcctctcaa cgatcagcgt 360  
catcgcttat ttctgcttct tcgtcatggg gtttgggcct atcccaaata ttctctgcgc 420  
ggagattttc cccacccctg tccgtggcat ctgcatalogcc atctgcgcgc taaccttctg 480  
gatcggcgac atcatcgtga catacactct ccccggtatg ctcaatgcca ttggtctcgc 540  
tggagtcctc ggcatatatg ccatcgtttgc tgtagctggcc tttgttattcg tctacatgaa 600  
ggtccctgag acaaaggca tgccccctgga ggtcatcacc gagttttcttct ctgtcggggc 660  
aaagcagggc aaggaagcca cggactagtt gctctgtatcc ggtatccgc gtcgctgggt 720  
gtaattttgt ggtgtataa ctactactac actggtaac ctgcgtatgt ttggtgaaga 780  
aacttcaaag agagcagata cggaaagactt tacatcgtga ggctgaattg tgcgtcgta 840  
ggccggctt tggaaagtagg atatgtactt agatcatctg ctctttcgc tttggaaactt 900  
tctatttgtt ttattcagaa tttcttgccc atgtaactag tgctgttatac acaatttatg 960  
tcgattatgt gtttgcctaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1009

<210> 16  
<211> 228  
<212> PRT  
<213> Triticum aestivum

<400> 16  
Glu Pro Gly Val Lys His Ala Leu Phe Val Gly Ile Gly Leu Gln Ile  
1 5 10 15  
Leu Gln Gln Phe Ala Gly Ile Asn Gly Val Leu Tyr Tyr Thr Pro Gln  
20 25 30  
Ile Leu Glu Gln Ala Gly Val Gly Val Leu Leu Ser Asn Ile Gly Leu  
35 40 45  
Ser Ser Ser Ser Ala Ser Ile Leu Ile Ser Ala Leu Thr Thr Leu Leu

BB-1163 US DIV Correct Sequence Listing  
50 55 60

Met Leu Pro Ser Ile Gly Ile Ala Met Arg Leu Met Asp Met Ser Gly  
65 70 75 80

Arg Arg Phe Leu Leu Leu Ser Thr Ile Pro Val Leu Ile Val Ala Leu  
85 90 95

Ala Val Leu Val Leu Val Asn Val Leu Asp Val Gly Thr Met Val His  
100 105 110

Ala Ala Leu Ser Thr Ile Ser Val Ile Val Tyr Phe Cys Phe Phe Val  
115 120 125

Met Gly Phe Gly Pro Ile Pro Asn Ile Leu Cys Ala Glu Ile Phe Pro  
130 135 140

Thr Ser Val Arg Gly Ile Cys Ile Ala Ile Cys Ala Leu Thr Phe Trp  
145 150 155 160

Ile Gly Asp Ile Ile Val Thr Tyr Thr Leu Pro Val Met Leu Asn Ala  
165 170 175

Ile Gly Leu Ala Gly Val Phe Gly Ile Tyr Ala Ile Val Cys Val Leu  
180 185 190

Ala Phe Val Phe Val Tyr Met Lys Val Pro Glu Thr Lys Gly Met Pro  
195 200 205

Leu Glu Val Ile Thr Glu Phe Phe Ser Val Gly Ala Lys Gln Gly Lys  
210 215 220

Glu Ala Thr Asp  
225

<210> 17  
<211> 615  
<212> DNA  
<213> Zea mays

<220>  
<221> unsure  
<222> (149)  
<223> n = a, c, g or t

<220>  
<221> unsure  
<222> (271)  
<223> n = a, c, g or t

<220>  
<221> unsure  
<222> (304)  
<223> n = a, c, g or t

<220>  
<221> unsure  
<222> (334)  
<223> n = a, c, g or t

<220>  
<221> unsure  
<222> (357)

BB-1163 US DIV Correct Sequence Listing

<223> n = a, c, g or t

<220>  
<221> unsure  
<222> (476)

<223> n = a, c, g or t

<220>  
<221> unsure  
<222> (599)

<223> n = a, c, g or t

<220>  
<221> unsure  
<222> (602)

<223> n = a, c, g or t

<400> 17  
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aggcaacgtc aagttcgccct tcgcctgcnc catcctcgcc tcaatgacct ccatccttct 180  
cggttatgtat atcggagtga tgagcggcgc gtcgttgtac atcaagaagg acctgaaaat 240  
cagcgacgtg aagctggaga tcctgatggg natcctcaac gtgtactcgc tcatacggtc 300  
gttngcggca gggcgacgt ccgactggat cggncccgat acaccatcg tttcgcnngcg 360  
gtgatcttct tcgcgggcgc ttccatgg gcttcgcccgt gaactactgg atgctcatgt 420  
tcgggcgtt cgtggccggg atcggcgtgg gctacgcgt catgatcgca accgtntaca 480  
cggccgaagt gtccccgcat cggccgcgg cttccgtacg tcgttcccg aggtgttcat 540  
cacttcggca tcctcttaggt acgtgtcaat aaggcttttc cgcttccgtt cgctggatng 600  
cnctaatgtc ggcatt 615

<210> 18  
<211> 167

<212> PRT

<213> Zea mays

<220>  
<221> UNSURE  
<222> (34)

<223> xaa = any amino acid

<220>  
<221> UNSURE  
<222> (85)

<223> xaa = any amino acid

<220>  
<221> UNSURE  
<222> (98)

<223> xaa = any amino acid

<220>  
<221> UNSURE  
<222> (112)

<223> xaa = any amino acid

<220>  
<221> UNSURE  
<222> (151)

<223> xaa = any amino acid

<400> 18  
Ser Arg Ala Gln Ser Glu Pro Ser Thr Met Ala Ser Ala Pro Leu Pro  
1 5 10 15

## BB-1163 US DIV Correct Sequence Listing

Ala Ala Ile Glu Pro Gly Lys Lys Gly Asn Val Lys Phe Ala Phe Ala  
 20 25 30  
 Cys Xaa Ile Leu Ala Ser Met Thr Ser Ile Leu Leu Gly Tyr Asp Ile  
 35 40 45  
 Gly Val Met Ser Gly Ala Ser Leu Tyr Ile Lys Lys Asp Leu Lys Ile  
 50 55 60  
 Ser Asp Val Lys Leu Glu Ile Leu Met Gly Ile Leu Asn Val Tyr Ser  
 65 70 75 80  
 Leu Ile Gly Ser Xaa Ala Ala Gly Arg Thr Ser Asp Trp Ile Gly Arg  
 85 90 95  
 Arg Xaa Thr Ile Val Phe Ala Ala Val Ile Phe Phe Ala Gly Ala Xaa  
 100 105 110  
 Leu Met Gly Phe Ala Val Asn Tyr Trp Met Leu Met Phe Gly Arg Phe  
 115 120 125  
 Val Ala Gly Ile Gly Val Gly Tyr Ala Leu Met Ile Ala Thr Val Tyr  
 130 135 140  
 Thr Ala Glu Val Ser Pro Xaa Ser Ala Arg Gly Phe Leu Thr Ser Phe  
 145 150 155 160  
 Pro Glu Val Phe Ile Thr Ser  
 165

<210> 19  
<211> 1914  
<212> DNA  
<213> Zea mays

<400>	19	gcacgaggca	cggcacctta	tctctaaccg	gagatcaaag	aagtagccgt	taacgatggc	60
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catatgtgcc		atcctggcct	ccatggcctc	tgtcatcctt	ggctatgaca	ttgggggtgat		180
gagtggagcg		gccatgtaca	tcaagaagga	cctgaatatc	acggacgtgc	agctggagat		240
cctgatcggg		atcctcagtc	tctactcgct	gttcggatcc	ttcgctggcg	cgcggacgtc		300
cgacaggatc		ggcgccgct	tgaccgtcgt	gttcgcccgt	gtcatcttct	tcgtgggctc		360
gttgctcatg		ggttccgccc	tcaactacgg	catgctcatg	gcgggcccgt	tcgtggccgg		420
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tggctacctg		tccaacttcg	cgttcgccgc	cctcccgctc	cacctcggt	ggcgcgtcat		600
gctcgccatt		ggcgcagttc	cgtccggcct	gctcgccgtc	ctggtgttct	gcatgcccga		660
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gacctctgcc		acgccagagg	aggccgcccga	gcggctggcc	gacatcaagg	ccgcggcggg		780
gattccgaag		ggcctcgacg	gggacgtagt	caccgtaccc	ggcaaggagc	aaggcggcgg		840
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gctctcgcc		gtgggtctcc	acttcttcca	gcaggcttct	ggcagcgtact	ccgtcgttcca		960
gtacagcgcc		cgcctgttca	agagcgccgg	gatcaccgac	gacaacaagc	tcctgggcgt		1020
cacctgcgca		gtgggcgtga	ccaagacgtt	cttcatcctg	gtggccacgt	tcctgcttgaa		1080
ccgcgcgggg		cgtcgccctc	tgctgctgat	cagcacggc	gggatgattg	tctcgctcat		1140
ctgcctcggg		tcggggctca	ccgtcgccgg	gcatcaccgg	gacaccaagg	tcgcgtgggc		1200
cgtcgccctg		tgcatcgct	caaccctgtc	ctacatcgcc	ttcttctcca	tcggcctcgg		1260
gcccatcacg		ggcgtgtaca	cctcggaaat	attcccgtg	caggtgcgcg	cgctgggctt		1320
cgcggtggt		gtggcgagca	accgcgtcac	cagcgccgtc	atctccatga	ccttcctgtc		1380
cctctccaag		gccatcacca	tcggcgccag	cttcttcctc	tactccggca	tcgcccgggt		1440
cgcttgggtt		ttcttcttca	cgtcctccc	ggagacacgc	ggccggacgc	tggaggagat		1500
qqqcaaqctq		ttcqgcatqc	cagacacggg	catggctgaa	gaagcagaag	acgcccgcagc		1560

BB-1163 US DIV Correct Sequence Listing

caaggagaag gtgggttgaac tgccttagcag caagtaggtg gctatcccag agcacaggc 1620  
aagtgaagta gatggacaag atcattgtct tttcaactaa ttagatggc aagaataact 1680  
aagactgccc tatgaggtgt cgtggttcaa ccagagatca ttctgctcct tttctttcc 1740  
cttcctttt cgagtaccat tcccattcgt cgtggtcagt acgatgttg gtcgttggg 1800  
gttagtgtg tcagagtccg cgtgtgctt gcaagccagg gctgaaccca caatcatcag 1860  
taacaaaaat tcttccgtt gcttgcaag caaaaaaaaaaa aaaaaaaaaaaa aaaa 1914

<210> 20  
<211> 513  
<212> PRT  
<213> Zea mays

<400> 20  
Met Ala Ser Asp Glu Leu Ala Lys Ala Val Glu Pro Arg Lys Lys Gly  
1 5 10 15  
Asn Val Lys Tyr Ala Ser Ile Cys Ala Ile Leu Ala Ser Met Ala Ser  
20 25 30  
Val Ile Leu Gly Tyr Asp Ile Gly Val Met Ser Gly Ala Ala Met Tyr  
35 40 45  
Ile Lys Lys Asp Leu Asn Ile Thr Asp Val Gln Leu Glu Ile Leu Ile  
50 55 60  
Gly Ile Leu Ser Leu Tyr Ser Leu Phe Gly Ser Phe Ala Gly Ala Arg  
65 70 75 80  
Thr Ser Asp Arg Ile Gly Arg Arg Leu Thr Val Val Phe Ala Ala Val  
85 90 95  
Ile Phe Phe Val Gly Ser Leu Leu Met Gly Phe Ala Val Asn Tyr Gly  
100 105 110  
Met Leu Met Ala Gly Arg Phe Val Ala Gly Val Gly Val Gly Tyr Gly  
115 120 125  
Gly Met Ile Ala Pro Val Tyr Thr Ala Glu Ile Ser Pro Ala Ala Ser  
130 135 140  
Arg Gly Phe Leu Thr Thr Phe Pro Glu Val Phe Ile Asn Ile Gly Ile  
145 150 155 160  
Leu Leu Gly Tyr Leu Ser Asn Phe Ala Phe Ala Arg Leu Pro Leu His  
165 170 175  
Leu Gly Trp Arg Val Met Leu Ala Ile Gly Ala Val Pro Ser Gly Leu  
180 185 190  
Leu Ala Leu Leu Val Phe Cys Met Pro Glu Ser Pro Arg Trp Leu Val  
195 200 205  
Leu Lys Gly Arg Leu Ala Asp Ala Arg Ala Val Leu Glu Lys Thr Ser  
210 215 220  
Ala Thr Pro Glu Glu Ala Ala Glu Arg Leu Ala Asp Ile Lys Ala Ala  
225 230 235 240  
Ala Gly Ile Pro Lys Gly Leu Asp Gly Asp Val Val Thr Val Pro Gly  
245 250 255  
Lys Glu Gln Gly Gly Glu Leu Gln Val Trp Lys Lys Leu Ile Leu  
260 265 270

BB-1163 US DIV Correct Sequence Listing

Ser Pro Thr Pro Ala Val Arg Arg Ile Leu Leu Ser Ala Val Gly Leu  
 275 280 285  
 His Phe Phe Gln Gln Ala Ser Gly Ser Asp Ser Val Val Gln Tyr Ser  
 290 295 300  
 Ala Arg Leu Phe Lys Ser Ala Gly Ile Thr Asp Asp Asn Lys Leu Leu  
 305 310 315 320  
 Gly Val Thr Cys Ala Val Gly Val Thr Lys Thr Phe Phe Ile Leu Val  
 325 330 335  
 Ala Thr Phe Leu Leu Asp Arg Ala Gly Arg Arg Pro Leu Leu Leu Ile  
 340 345 350  
 Ser Thr Gly Gly Met Ile Val Ser Leu Ile Cys Leu Gly Ser Gly Leu  
 355 360 365  
 Thr Val Ala Gly His His Pro Asp Thr Lys Val Ala Trp Ala Val Ala  
 370 375 380  
 Leu Cys Ile Ala Ser Thr Leu Ser Tyr Ile Ala Phe Phe Ser Ile Gly  
 385 390 395 400  
 Leu Gly Pro Ile Thr Gly Val Tyr Thr Ser Glu Ile Phe Pro Leu Gln  
 405 410 415  
 Val Arg Ala Leu Gly Phe Ala Val Gly Val Ala Ser Asn Arg Val Thr  
 420 425 430  
 Ser Ala Val Ile Ser Met Thr Phe Leu Ser Leu Ser Lys Ala Ile Thr  
 435 440 445  
 Ile Gly Gly Ser Phe Phe Leu Tyr Ser Gly Ile Ala Ala Val Ala Trp  
 450 455 460  
 Val Phe Phe Phe Thr Cys Leu Pro Glu Thr Arg Gly Arg Thr Leu Glu  
 465 470 475 480  
 Glu Met Gly Lys Leu Phe Gly Met Pro Asp Thr Gly Met Ala Glu Glu  
 485 490 495  
 Ala Glu Asp Ala Ala Ala Lys Glu Lys Val Val Glu Leu Pro Ser Ser  
 500 505 510  
 Lys

<210> 21  
 <211> 2017  
 <212> DNA  
 <213> Oryza sativa

<400> 21  
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 cagagcgagc ctcctcctcc tctgcaccac cggagatggc ttccgcccgc ctgccggagg 120  
 ccgtcgccgc gaagaagaag ggcaacgtcc gtttcgcctt cgcctgcgcc atcctcgct 180  
 ccatgacctc catcctcctc ggctacgata tcgggggtat gagcggggcg tcgctgtaca 240  
 tcaagaagga cttcaacatc agtgacggga aggtggaggt tctcatggc atactgaacc 300  
 tctactcgct catcggtctcc ttgcggccgg ggcggacgtc ggactggatc ggccggcggt 360  
 acaccatcgt gttcgccgcc gtcattattct tcgcgggggs gttcctcatg gggttcgccc 420  
 tcaactacgc catgctcatg ttgcggccgt tcgtggccgg catcggcgtg ggctacgcgc 480

BB-1163 US DIV Correct Sequence Listing

tcatgatcgc	gccggtgtac	accggcgagg	tgtcgccggc	gtcgccgcgt	ggcttcctga	540
cgtcgcccc	ggaggggttgc	atcaacttcg	gcatcctgct	cgggtacgtc	tcgaactatg	600
ctttctcccg	cttgcggctg	aacctcggt	ggcgcatcat	gctcgccatc	ggcgccggcgc	660
cgtccgtgct	gctcgccctc	atgggtctcg	gcatgcccga	gtcgccgcgg	tggctggtca	720
tgaaggacg	cctcgccggac	gccaagggtgg	tgctggagaa	gacctccgac	acggcggagg	780
aggccgcgg	gcccctggcc	gacatcaagg	ccgcccgg	catcccttag	gagctcgacg	840
gacgtgggt	gaccgtcccc	aagagaggg	gcggaaacga	gaagcgggtg	tggaggagc	900
tcatcctgtc	cccgaccctcg	gccatgcggc	gcatcctgct	gtccgggatc	ggcatccact	960
tcttcagca	tgcgttggc	attcaactccg	tcgtcttcta	cagccctctc	gtgttcaaga	1020
gccccggatt	aacgaacgcac	aaacacttct	tgggcaccac	ttggccgttc	ggtgtcacca	1080
agaggcttt	catcttgg	gacacttct	tcatcgacgg	cgtcgggccc	cggccgctgt	1140
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tcgtcgccca	gcaccccgac	gccaagatac	tttggccat	cggcctaagc	atcgccctca	1260
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cggagatctt	cccgctccag	gtgcgcgc	tgggtctgctc	gctcggcgtc	gccgccaacc	1380
gcgtcaccag	cggcgtcattc	tccatgaccc	tcctgtcgct	gtccaaggcc	atcaccatcg	1440
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acctcccgga	gaccgcggc	cggacgctgg	aggagatgag	caagctgttc	ggcgacacgg	1560
ccgcccgcctc	ggaatcagac	gagccagcca	aggagaagaa	gaaggtggaa	atggccgcca	1620
ctaactgatc	aaactaaccg	caaaatcacc	aaatcctaag	gttttcttg	aaaaaacgtg	1680
tgctgtactg	gctagctagc	aagttagtc	agcaacgtgg	gaagattcgc	tgatccggcg	1740
ttgctggaga	gacggcccg	gacgaccaa	agctgagctc	cagctcgaga	cttcttaaaa	1800
tcatcttcaa	gtacatggat	tttattttgc	tcttgcttt	gtccgtaaaa	gttgtactat	1860
gcgatgaaga	ataccagtt	gtacaaggc	tgaggttgg	tgtagctact	agaagtgtca	1920
gtcacgttgt	tcttggtaaga	aatgttaac	tgttaattaa	gcagtattgt	tgcagtaatc	1980
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa			2017

<210> 22

<211> 510

<212> PRT

<213> Oryza sativa

<220>

<221> UNSURE

<222> (102)

<223> Xaa = any amino acid

<400> 22

Met	Ala	Ser	Ala	Ala	Leu	Pro	Glu	Ala	Val	Ala	Pro	Lys	Lys	Lys	Gly
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Asn	Val	Arg	Phe	Ala	Phe	Ala	Cys	Ala	Ile	Leu	Ala	Ser	Met	Thr	Ser
									25					30	

Ile	Leu	Leu	Gly	Tyr	Asp	Ile	Gly	val	Met	Ser	Gly	Ala	Ser	Leu	Tyr
								40					45		

Ile	Lys	Lys	Asp	Phe	Asn	Ile	Ser	Asp	Gly	Lys	val	Glu	val	Leu	Met
									55				60		

Gly	Ile	Leu	Asn	Leu	Tyr	Ser	Leu	Ile	Gly	Ser	Phe	Ala	Ala	Gly	Arg
								65					75		80

Thr	Ser	Asp	Trp	Ile	Gly	Arg	Arg	Tyr	Thr	Ile	val	Phe	Ala	Ala	val
									85				90		95

Ile	Phe	Phe	Ala	Gly	Xaa	Phe	Leu	Met	Gly	Phe	Ala	val	Asn	Tyr	Ala
								100				105		110	

Met	Leu	Met	Phe	Gly	Arg	Phe	Val	Ala	Gly	Ile	Gly	val	Gly	Tyr	Ala
												115		120	

Leu	Met	Ile	Ala	Pro	Val	Tyr	Thr	Ala	Glu	Val	Ser	Pro	Ala	Ser	Ala

BB-1163 US DIV Correct Sequence Listing  
130                    135                    140

Arg Gly Phe Leu Thr Ser Phe Pro Glu Val Phe Ile Asn Phe Gly Ile  
145                    150                    155                    160  
Leu Leu Gly Tyr Val Ser Asn Tyr Ala Phe Ser Arg Leu Pro Leu Asn  
165                    170                    175  
Leu Gly Trp Arg Ile Met Leu Gly Ile Gly Ala Ala Pro Ser Val Leu  
180                    185                    190  
Leu Ala Leu Met Val Leu Gly Met Pro Glu Ser Pro Arg Trp Leu Val  
195                    200                    205  
Met Lys Gly Arg Leu Ala Asp Ala Lys Val Val Leu Glu Lys Thr Ser  
210                    215                    220  
Asp Thr Ala Glu Glu Ala Ala Glu Arg Leu Ala Asp Ile Lys Ala Ala  
225                    230                    235                    240  
Ala Gly Ile Pro Glu Glu Leu Asp Gly Asp Val Val Thr Val Pro Lys  
245                    250                    255  
Arg Gly Ser Gly Asn Glu Lys Arg Val Trp Lys Glu Leu Ile Leu Ser  
260                    265                    270  
Pro Thr Pro Ala Met Arg Arg Ile Leu Leu Ser Gly Ile Gly Ile His  
275                    280                    285  
Phe Phe Gln His Ala Leu Gly Ile His Ser Val Val Phe Tyr Ser Pro  
290                    295                    300  
Leu Val Phe Lys Ser Pro Gly Leu Thr Asn Asp Lys His Phe Leu Gly  
305                    310                    315                    320  
Thr Thr Trp Pro Phe Gly Val Thr Lys Arg Leu Phe Ile Leu Leu Ala  
325                    330                    335  
Thr Phe Phe Ile Asp Gly Val Gly Arg Arg Pro Leu Leu Leu Gly Ser  
340                    345                    350  
Thr Gly Gly Ile Ile Leu Ser Leu Ile Gly Leu Gly Ala Gly Leu Thr  
355                    360                    365  
Val Val Gly Gln His Pro Asp Ala Lys Ile Pro Trp Ala Ile Gly Leu  
370                    375                    380  
Ser Ile Ala Ser Thr Leu Ala Tyr Val Ala Phe Phe Ser Ile Gly Leu  
385                    390                    395                    400  
Gly Pro Ile Thr Trp Val Tyr Ser Ser Glu Ile Phe Pro Leu Gln Val  
405                    410                    415  
Arg Ala Leu Gly Cys Ser Leu Gly Val Ala Ala Asn Arg Val Thr Ser  
420                    425                    430  
Gly Val Ile Ser Met Thr Phe Leu Ser Leu Ser Lys Ala Ile Thr Ile  
435                    440                    445  
Gly Gly Ser Phe Phe Leu Tyr Ser Gly Ile Ala Ala Leu Ala Trp Val  
450                    455                    460  
Phe Phe Tyr Thr Tyr Leu Pro Glu Thr Arg Gly Arg Thr Leu Glu Glu

BB-1163 US DIV Correct Sequence Listing  
70 475 480

Met Ser Lys Leu Phe Gly Asp Thr Ala Ala Ala Ser Glu Ser Asp Glu  
485 490 495

Pro Ala Lys Glu Lys Lys Lys Val Glu Met Ala Ala Thr Asn  
500 505 510

<210> 23  
<211> 1853  
<212> DNA  
<213> Glycine max

<400>	23	ttctctcttc	acatatcatc	atacttagat	agtcagatac	atcacccaat	60
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aattaaatta		ctgcggatat	tcagctaatt	aaactaagtc	actaagatga	ctgagggaaa	180
atttccctt		gctgcagaag	ctcataagac	acttcaggat	ttcgatcctc	caaagaagcg	240
gctagttgaa		aagtatgctt	ttgcttgc	tatgctggcc	tccatgactt	ccatcttgct	300
caaaaggaac		attggagtgta	tgagtggagc	agccatatac	ataaaaaaggg	acctgaaagt	360
tggttatgtat		caaatcgaga	tcctgctcgg	aatcatcaac	ctatactctc	tgataggctc	420
ctcggacgag		ggcagaacct	ccgactggat	aggtccccgt	tacacgattg	tttgcgccgg	480
atgtctcgcc		tttgtcggag	cacttctcat	gggtttctcc	cccaattatt	ccttctcat	540
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gtttggccgt		gtctccccgg	cctcctctcg	tggcttcctc	acttccttcc	ctgaggtatt	660
caccgcccag		gggatattaa	ttggatacat	atcaaactat	gcattttcga	agctgacact	720
tattaatgga		tggcgaatga	tgcttggagt	tggtgcaata	ccttcggtac	tcctaacagt	780
aaaggtggga		gcgtatgccgg	agtccccaaag	gtggcttgc	atgaggggtc	gtttgggaga	840
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ggcaagaaaa		caagccgcag	ggatccccga	gagttgcaac	gacgacgtcg	ttcaggtaaa	960
ggaaatcaaa		aacggtgaag	gtgtatggaa	agagctcttc	ctctatccaa	cgcggcaat	1020
taaacaaaagc		gtaatcgctg	cccttggtat	tcacttcttc	caacaagcgt	cgggcgtaga	1080
tcgtcacatc		ttgtacagcc	ccaggatctt	cgaaaaggct	gggattacaa	acgacacgca	1140
cgcgcgtgtt		gcaaccgtgg	ccgttggatt	cgttaagacc	gtgttcatct	tggcggctac	1200
taagcttctt		gaccgcgtgg	gtcgtcgcc	gttgttattt	tctagtgtcg	gcggcatgtt	1260
gtttagtttg		ctcacgctt	cgatcagcct	cactgttatt	gatcattcgg	agaggaatt	1320
gctctcgctt		gttggatcga	gcataccat	ggtgttggct	tacgtggcca	cgttctccat	1380
aatgtgggccc		cccatcacgt	gggtctata	ttctgagatc	ttcccggttga	ggctgcgggc	1440
cgggtgcgggt		gccgcgggag	ttgcggtgaa	taggaccact	agcgcgggt	tctcaatgac	1500
gcarggtgcg		ctcactagag	ccatcactat	tggtgagct	ttcttcctt	attgtggcat	1560
ttttctgtcc		gggtggatat	tcttttacac	cgtcttgcc	gagacccggg	aaaaaacgct	1620
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cgaagacatg		aatgggcaag	tagcacaagt	ccagcttagga	accaatgtcc	aaacttgaaa	1740
agaaaaatgag		gggacatcca	gtaatagtga	agtaatttcg	tgatttttt	tttggttttt	1800
aatgagtatt		ctagtttttc	aaatcaaaac	gagaagttaa	agtaaaaaaa	aaa	1853

<210> 24  
<211> 523  
<212> PRT  
<213> Glycine max

<400> 24  
Met Thr Glu Gly Lys Leu Val Glu Ala Ala Glu Ala His Lys Thr Leu  
1 5 10 15

Gln Asp Phe Asp Pro Pro Lys Lys Arg Lys Arg Asn Lys Tyr Ala Phe  
20 25 30

Ala Cys Ala Met Leu Ala Ser Met Thr Ser Ile Leu Leu Gly Tyr Asp  
35 40 45

Ile Gly Val Met Ser Gly Ala Ala Ile Tyr Ile Lys Arg Asp Leu Lys  
50 55 60

BB-1163 US DIV Correct Sequence Listing

val Ser Asp Glu Gln Ile Glu Ile Leu Leu Gly Ile Ile Asn Leu Tyr  
 65 70 75 80  
 Ser Leu Ile Gly Ser Cys Leu Ala Gly Arg Thr Ser Asp Trp Ile Gly  
 85 90 95  
 Pro Arg Tyr Thr Ile Val Phe Ala Gly Thr Ile Phe Phe Val Gly Ala  
 100 105 110  
 Leu Leu Met Gly Phe Ser Pro Asn Tyr Ser Phe Leu Met Phe Gly Arg  
 115 120 125  
 Phe Val Ala Gly Ile Gly Ile Gly Tyr Ala Leu Met Ile Ala Pro Val  
 130 135 140  
 Tyr Thr Ala Glu Val Ser Pro Ala Ser Ser Arg Gly Phe Leu Thr Ser  
 145 150 155 160  
 Phe Pro Glu Val Phe Ile Asn Gly Gly Ile Leu Ile Gly Tyr Ile Ser  
 165 170 175  
 Asn Tyr Ala Phe Ser Lys Leu Thr Leu Lys Val Gly Trp Arg Met Met  
 180 185 190  
 Leu Gly Val Gly Ala Ile Pro Ser Val Leu Leu Thr Val Gly Val Leu  
 195 200 205  
 Ala Met Pro Glu Ser Pro Arg Trp Leu Val Met Arg Gly Arg Leu Gly  
 210 215 220  
 Glu Ala Arg Lys Val Leu Asn Lys Thr Ser Asp Ser Lys Glu Glu Ala  
 225 230 235 240  
 Gln Leu Arg Leu Ala Glu Ile Lys Gln Ala Ala Gly Ile Pro Glu Ser  
 245 250 255  
 Cys Asn Asp Asp Val Val Gln Val Asn Lys Gln Ser Asn Gly Glu Gly  
 260 265 270  
 val Trp Lys Glu Leu Phe Leu Tyr Pro Thr Pro Ala Ile Arg His Ile  
 275 280 285  
 val Ile Ala Ala Leu Gly Ile His Phe Phe Gln Gln Ala Ser Gly Val  
 290 295 300  
 Asp Ala Val Val Leu Tyr Ser Pro Arg Ile Phe Glu Lys Ala Gly Ile  
 305 310 315 320  
 Thr Asn Asp Thr His Lys Leu Leu Ala Thr Val Ala Val Gly Phe Val  
 325 330 335  
 Lys Thr Val Phe Ile Leu Ala Ala Thr Phe Thr Leu Asp Arg Val Gly  
 340 345 350  
 Arg Arg Pro Leu Leu Leu Ser Ser Val Gly Gly Met Val Leu Ser Leu  
 355 360 365  
 Leu Thr Leu Ala Ile Ser Leu Thr Val Ile Asp His Ser Glu Arg Lys  
 370 375 380  
 Leu Met Trp Ala Val Gly Ser Ser Ile Ala Met Val Leu Ala Tyr Val  
 385 390 395 400

BB-1163 US DIV Correct Sequence Listing

Ala Thr Phe Ser Ile Gly Ala Gly Pro Ile Thr Trp Val Tyr Ser Ser  
405 410 415

Glu Ile Phe Pro Leu Arg Leu Arg Ala Gln Gly Ala Ala Ala Gly Val  
420 425 430

Ala Val Asn Arg Thr Thr Ser Ala Val Val Ser Met Thr Phe Leu Ser  
435 440 445

Leu Thr Arg Ala Ile Thr Ile Gly Gly Ala Phe Phe Leu Tyr Cys Gly  
450 455 460

Ile Ala Thr Val Gly Trp Ile Phe Phe Tyr Thr Val Leu Pro Glu Thr  
465 470 475 480

Arg Gly Lys Thr Leu Glu Asp Met Glu Gly Ser Phe Gly Thr Phe Arg  
485 490 495

Ser Lys Ser Asn Ala Ser Lys Ala Val Glu Asn Glu Asn Gly Gln Val  
500 505 510

Ala Gln Val Gln Leu Gly Thr Asn Val Gln Thr  
515 520

<210> 25

<211> 2089

<212> DNA

<213> Triticum aestivum

<400> 25

agcaccacta	aactatacac	aaggaggacc	tcgtcgccat	aatcctcagg	cagcgagcag	60
aggggcgtcg	tcgacgatgg	accgcgccgc	actcccggcg	gccgtcgagc	ccaagaagaa	120
gggcaacgtg	aggttcgccct	tcgcctgcgc	catcctcgcc	tccatgacct	ccatcctcct	180
cggctacgac	atcggcgtga	tgagcggagc	gtcgctgtac	atccagaagg	atctgaagat	240
caacgacacc	cagctggagg	tcctcatggg	catcctcaac	gtgtactcgc	tcattggctc	300
cttcgcggcg	gggcggacgt	ccgactggat	cggccggcgc	ttcaccatcg	tcttcgcccgc	360
cgtcatcttc	ttcgcgggchg	ccctcatcat	gggcttctcc	gtcaactacg	ccatgctcat	420
gttcgggcgc	ttcgtggccg	gcatcggcgt	ggggtacgct	ctcatgatcg	cggccgtgaa	480
cacgggcgag	gtgtcccccg	cgtctgccc	tggggttctc	acatccttcc	cggagggtgtt	540
catcaacttc	ggcatcctcc	tcggatatgt	ctccaacttc	gccttcgccc	gcctctccct	600
ccgcctcggc	tggcgcatta	tgctcggcat	aggcgcggtg	ccgtccgtcc	tgctcgcgtt	660
catggtgc	ggcatgccc	agtctcccc	gtggctcg	atgaaggccc	gtctcgcgga	720
cgc	caagggtt	gtgcttgcca	agacgtccga	cacgcccggaa	gaggccgccc	780
cgacattaag	actgcccggc	gcatccctct	gggcctcgac	ggcgcacgtgg	tcccccgtgcc	840
caaaaacaaa	ggaagcagcg	aggagaagcg	cgtttgaag	gacctcatcc	tgtcaccgac	900
catagccatg	cgccacatcc	tcatcggcggg	aatcggcattc	cacttcttcc	agcagtcttc	960
gggcatcgac	gccgtcg	tctacagccc	gctagtttc	aagagcggcc	gcatcacggg	1020
cgacagccgt	ctccgcggca	ccaccgtggc	gttcggggcc	accaatacgg	tcttcatcct	1080
ggtggccacc	ttcctcctcg	accgcattcg	ccggcggcc	ctggtgctga	ccagcacggg	1140
cggcatgctc	gtctccttag	tgggcctcgc	gacggggctc	accgtcatca	gccgcccaccc	1200
gjacgagaag	atcacctggg	ccatcgtcct	gtgcattttc	tgcattatgg	cctacgtggc	1260
cttcttctcc	atcggcctcg	gccccatcac	gtgggtgtac	agctcggaga	tcttcccgt	1320
gcacgtgcgc	g	gctccctggg	cgtggccgtc	aaccgcctga	ccagcggcgt	1380
gatctccatg	accttcat	cgctgtccaa	ggccatgacc	atcggcggcg	ccttcttcct	1440
cttcgcggc	atcgcctcat	tcgcattgggt	gttcttcttc	gccttacactc	cggagacccg	1500
cggccgcacg	ctggaggaca	tgagctcg	gttcggcaac	acggccacgc	acaaggcagg	1560
cggccgcggaa	gcccacgacg	acgccccgg	gaagaagggt	gaaatggccg	ccaccaactg	1620
accgcaagtt	ggcagatcgc	gatgcgaaga	cttgcgtgt	atccgtctcg	gctagctagc	1680
tgccacaagg	ccacatagat	gacgaagt	cgtggaaaga	ttcgctgatc	cggccggagc	1740
tgccggaggg	cgacggcaag	ctccagctcg	atcgagacgt	taatggcttc	ttaaatgtgc	1800
taagtttaat	gtttcgctct	ttgggtttgt	ccgggttaggt	cgtgagcaat	ccggtagtgc	1860
cgatgccaag	gctaatcgac	gccggacgga	ctagactact	gttagact	gtagagggtgt	1920

BB-1163 US DIV Correct Sequence Listing

accgttgcta cttccgtggc gtttgcgtgc atgatttagga gagaaaaactg gcgggtggtc 1980  
gaggactcta cctgccatc gagtgagtca agcgagccac ggaaaatgtg taagaaaaaa 2040  
atattaagta tgtgtattgt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2089

<210> 26

<211> 539

<212> PRT

<213> Triticum aestivum

<400> 26

Ala Pro Leu Asn Tyr Thr Gln Gly Gly Pro Arg Arg His Asn Pro Gln  
1 5 10 15

Ala Ala Ser Arg Gly Ala Ser Ser Thr Met Asp Arg Ala Ala Leu Pro  
20 25 30

Ala Ala val Glu Pro Lys Lys Lys Gly Asn val Arg Phe Ala Phe Ala  
35 40 45

Cys Ala Ile Leu Ala Ser Met Thr Ser Ile Leu Leu Gly Tyr Asp Ile  
50 55 60

Gly Val Met Ser Gly Ala Ser Leu Tyr Ile Gln Lys Asp Leu Lys Ile  
65 70 75 80

Asn Asp Thr Gln Leu Glu Val Leu Met Gly Ile Leu Asn Val Tyr Ser  
85 90 95

Leu Ile Gly Ser Phe Ala Ala Gly Arg Thr Ser Asp Trp Ile Gly Arg  
100 105 110

Arg Phe Thr Ile Val Phe Ala Ala Val Ile Phe Phe Ala Gly Ala Leu  
115 120 125

Ile Met Gly Phe Ser Val Asn Tyr Ala Met Leu Met Phe Gly Arg Phe  
130 135 140

Val Ala Gly Ile Gly Val Gly Tyr Ala Leu Met Ile Ala Pro Val Asn  
145 150 155 160

Thr Gly Glu Val Ser Pro Ala Ser Ala Arg Gly Val Leu Thr Ser Phe  
165 170 175

Pro Glu Val Phe Ile Asn Phe Gly Ile Leu Leu Gly Tyr Val Ser Asn  
180 185 190

Phe Ala Phe Ala Arg Leu Ser Leu Arg Leu Gly Trp Arg Ile Met Leu  
195 200 205

Gly Ile Gly Ala Val Pro Ser Val Leu Leu Ala Phe Met Val Leu Gly  
210 215 220

Met Pro Glu Ser Pro Arg Trp Leu Val Met Lys Gly Arg Leu Ala Asp  
225 230 235 240

Ala Lys Val Val Leu Ala Lys Thr Ser Asp Thr Pro Glu Glu Ala Ala  
245 250 255

Glu Arg Ile Ala Asp Ile Lys Thr Ala Ala Gly Ile Pro Leu Gly Leu  
260 265 270

Asp Gly Asp Val Val Pro Val Pro Lys Asn Lys Gly Ser Ser Glu Glu  
275 280 285

BB-1163 US DIV Correct Sequence Listing

Lys Arg Val Leu Lys Asp Leu Ile Leu Ser Pro Thr Ile Ala Met Arg  
 290 295 300  
 His Ile Leu Ile Ala Gly Ile Gly Ile His Phe Phe Gln Gln Ser Ser  
 305 310 315 320  
 Gly Ile Asp Ala Val Val Leu Tyr Ser Pro Leu Val Phe Lys Ser Ala  
 325 330 335  
 Gly Ile Thr Gly Asp Ser Arg Leu Arg Gly Thr Thr Val Ala Val Gly  
 340 345 350  
 Ala Thr Asn Thr Val Phe Ile Leu Val Ala Thr Phe Leu Leu Asp Arg  
 355 360 365  
 Ile Arg Arg Arg Pro Leu Val Leu Thr Ser Thr Gly Gly Met Leu Val  
 370 375 380  
 Ser Leu Val Gly Leu Ala Thr Gly Leu Thr Val Ile Ser Arg His Pro  
 385 390 395 400  
 Asp Glu Lys Ile Thr Trp Ala Ile Val Leu Cys Ile Phe Cys Ile Met  
 405 410 415  
 Ala Tyr Val Ala Phe Phe Ser Ile Gly Leu Gly Pro Ile Thr Trp Val  
 420 425 430  
 Tyr Ser Ser Glu Ile Phe Pro Leu His Val Arg Ala Leu Gly Cys Ser  
 435 440 445  
 Leu Gly Val Ala Val Asn Arg Leu Thr Ser Gly Val Ile Ser Met Thr  
 450 455 460  
 Phe Ile Ser Leu Ser Lys Ala Met Thr Ile Gly Gly Ala Phe Phe Leu  
 465 470 475 480  
 Phe Ala Gly Ile Ala Ser Phe Ala Trp Val Phe Phe Phe Ala Tyr Leu  
 485 490 495  
 Pro Glu Thr Arg Gly Arg Thr Leu Glu Asp Met Ser Ser Leu Phe Gly  
 500 505 510  
 Asn Thr Ala Thr His Lys Gln Gly Ala Ala Glu Ala Asp Asp Asp Ala  
 515 520 525  
 Gly Glu Lys Lys Val Glu Met Ala Ala Thr Asn  
 530 535

<210> 27  
 <211> 1872  
 <212> DNA  
 <213> Triticum aestivum

<400> 27  
 gcacgagctc atcactaggc tgtcagtctg tctgttcaac gaacgatcag ttcgtcctaa 60  
 gcagatggaa atgtctccgg aaagaaaagg agcggaggac aaggaagaag gatcgaggat 120  
 ggcttctgct gcgctccgg agccgggggc agtccatcca aggaacaagg gcaatttcaa 180  
 gtacgccttc acctgcgccc tctgtgcttc catggccacc atcgtcctcg gctacgacgt 240  
 tggggtgatg agcgggtgcgt cgctgtacat caagagggac ctgcagatca cggacgtgca 300  
 gctggagatc atgatgggca tcctgagcgt gtacgcgctc atcgggtct tcctcgccgc 360  
 gaggacgtcc gactgggtcg gccgccgcgt caccgtcgcc ttccgcggccg ccatcttcaa 420  
 caacggctcc ttgctcatgg gcttcgcgtt caactacgcc atgctcatgg tcgggcgtt 480

BB-1163 US DIV Correct Sequence Listing

cgtcaccgga	atcggcgtgg	gctacgccat	catggtcgcg	ccagtgtaca	cgcggaggt	540
gtccccggcg	tcggcccgcg	gcttcctcac	gtctttcacc	gagggttca	tcaatgtggg	600
catcctcctt	ggctacgtct	ccaactacgc	cttcgcgcgc	ctcccgtcc	acctcagctg	660
gcmcgtcatg	ctcggcatcg	gcccgtccc	gtccgcctg	cttgcgtca	tgggtttcgg	720
catgccggag	tctcctcgct	ggctcgcat	gaaaggccgc	ctcgccgacg	ccagggccgt	780
tctggccaag	acctccgaca	cgccggagga	ggccgtggag	cgccttgacc	agatcaaggc	840
tgccgcccgc	atcccttaggg	aacttgcgg	cgacgtggtc	gtcatgccta	agacaaaagg	900
cggccaggag	aagcaggtgt	ggaaggagct	catctttcg	ccgaccccag	ccatgcggcg	960
catactgctc	gcggcgctcg	gcatccattt	ctttcagcag	gcgacgggt	ccgactccgt	1020
cgtgctctat	agcccacgcg	tgttccagag	cgcgggcattc	accggcgaca	accacctgct	1080
cggcgccaca	tgcgccatgg	gggtcatgaa	gacgcttttc	atcctggtgg	ccacgttcca	1140
gctcgaccgc	gtcggcaggc	ggccgctgct	gctgaccagc	acggccggca	tgctcgccgt	1200
tctcatcggc	ctcgggacgg	gcctcaccgt	cgtgggtcg	cacccggacg	ccaaggtccc	1260
gtgggccatc	ggcctgtgca	tcgtgtccat	cttggcctac	gtgtccttct	tctccatcgg	1320
cctcgggccc	ctcaccagcg	tgtacacctc	ggaggtcttc	ccactgcggg	tgcgcgcgt	1380
gggcttcgcg	ctgggcacgt	catgcaaccg	cgtcaccagc	gccgcggct	ccatgtcctt	1440
cctgtccttg	tccaggcca	tcaccatcg	cggcagcttc	ttcctgtacg	ccggcatcgc	1500
ggcgatagga	tggattttct	tcttcacctt	cattccggag	acgcgtggcc	tgcgcgtcga	1560
ggagataggg	aagctttcg	gcatgacgga	cacggccgtc	gaagcccaag	acaccgcccc	1620
gaaagacaag	gcgaaagtag	gggagatgaa	ctagtgagct	agacgtcaac	caactgttac	1680
cgatgtacta	ccatagagat	gtatctgatc	aacgtggcaa	tataagtgtc	acggactctt	1740
gtgtctcatt	gatggattgt	ttggataaaa	tttcaagaga	attgtttcaa	gtttggatcc	1800
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1860
aaaaaaaaaa	aa					1872

<210> 28

<211> 529

<212> PRT

<213> *Triticum aestivum*

<400> 28

Met Lys Met Ser Pro Glu Arg Lys Gly Ala Glu Asp Lys Glu Glu Gly  
1 5 10 15

Ser Arg Met Ala Ser Ala Ala Leu Pro Glu Pro Gly Ala Val His Pro  
20 25 30

Arg Asn Lys Gly Asn Phe Lys Tyr Ala Phe Thr Cys Ala Leu Cys Ala  
35 40 45

Ser Met Ala Thr Ile Val Leu Gly Tyr Asp Val Gly Val Met Ser Gly  
50 55 60

Ala Ser Leu Tyr Ile Lys Arg Asp Leu Gln Ile Thr Asp Val Gln Leu  
65 70 75 80

Glu Ile Met Met Gly Ile Leu Ser Val Tyr Ala Leu Ile Gly Ser Phe  
85 90 95

Leu Gly Ala Arg Thr Ser Asp Trp Val Gly Arg Arg Val Thr Val Val  
100 105 110

Phe Ala Ala Ala Ile Phe Asn Asn Gly Ser Leu Leu Met Gly Phe Ala  
115 120 125

Val Asn Tyr Ala Met Leu Met Val Gly Arg Phe Val Thr Gly Ile Gly  
130 135 140

Val Gly Tyr Ala Ile Met Val Ala Pro Val Tyr Thr Pro Glu Val Ser  
145 150 155 160

Pro Ala Ser Ala Arg Gly Phe Leu Thr Ser Phe Thr Glu Val Phe Ile  
165 170 175

BB-1163 US DIV Correct Sequence Listing

Asn Val Gly Ile Leu Leu Gly Tyr Val Ser Asn Tyr Ala Phe Ala Arg  
180 185 190  
Leu Pro Leu His Leu Ser Trp Arg Val Met Leu Gly Ile Gly Ala Val  
195 200 205  
Pro Ser Ala Leu Leu Ala Leu Met Val Phe Gly Met Pro Glu Ser Pro  
210 215 220  
Arg Trp Leu Val Met Lys Gly Arg Leu Ala Asp Ala Arg Ala Val Leu  
225 230 235 240  
Ala Lys Thr Ser Asp Thr Pro Glu Glu Ala Val Glu Arg Leu Asp Gln  
245 250 255  
Ile Lys Ala Ala Ala Gly Ile Pro Arg Glu Leu Asp Gly Asp Val Val  
260 265 270  
Val Met Pro Lys Thr Lys Gly Gly Gln Glu Lys Gln Val Trp Lys Glu  
275 280 285  
Leu Ile Phe Ser Pro Thr Pro Ala Met Arg Arg Ile Leu Leu Ala Ala  
290 295 300  
Leu Gly Ile His Phe Phe Gln Gln Ala Thr Gly Ser Asp Ser Val Val  
305 310 315 320  
Leu Tyr Ser Pro Arg Val Phe Gln Ser Ala Gly Ile Thr Gly Asp Asn  
325 330 335  
His Leu Leu Gly Ala Thr Cys Ala Met Gly Val Met Lys Thr Leu Phe  
340 345 350  
Ile Leu Val Ala Thr Phe Gln Leu Asp Arg Val Gly Arg Arg Pro Leu  
355 360 365  
Leu Leu Thr Ser Thr Ala Gly Met Leu Ala Cys Leu Ile Gly Leu Gly  
370 375 380  
Thr Gly Leu Thr Val Val Gly Arg His Pro Asp Ala Lys Val Pro Trp  
385 390 395 400  
Ala Ile Gly Leu Cys Ile Val Ser Ile Leu Ala Tyr Val Ser Phe Phe  
405 410 415  
Ser Ile Gly Leu Gly Pro Leu Thr Ser Val Tyr Thr Ser Glu Val Phe  
420 425 430  
Pro Leu Arg Val Arg Ala Leu Gly Phe Ala Leu Gly Thr Ser Cys Asn  
435 440 445  
Arg Val Thr Ser Ala Ala Val Ser Met Ser Phe Leu Ser Leu Ser Lys  
450 455 460  
Ala Ile Thr Ile Gly Gly Ser Phe Phe Leu Tyr Ala Gly Ile Ala Ala  
465 470 475 480  
Ile Gly Trp Ile Phe Phe Phe Thr Phe Ile Pro Glu Thr Arg Gly Leu  
485 490 495  
Pro Leu Glu Glu Ile Gly Lys Leu Phe Gly Met Thr Asp Thr Ala Val  
500 505 510

BB-1163 US DIV Correct Sequence Listing

Glu Ala Gln Asp Thr Ala Thr Lys Asp Lys Ala Lys Val Gly Glu Met  
515 520 525

Asn

<210> 29  
<211> 729  
<212> PRT  
<213> Arabidopsis thaliana

<400> 29  
Met Ser Gly Ala Val Leu Val Ala Ile Ala Ala Ala Val Gly Asn Leu  
1 5 10 15  
Leu Gln Gly Trp Asp Asn Ala Thr Ile Ala Gly Ala Val Leu Tyr Ile  
20 25 30  
Lys Lys Glu Phe Asn Leu Glu Ser Asn Pro Ser Val Glu Gly Leu Ile  
35 40 45  
Val Ala Met Ser Leu Ile Gly Ala Thr Leu Ile Thr Thr Cys Ser Gly  
50 55 60  
Gly Val Ala Asp Trp Leu Gly Arg Arg Pro Met Leu Ile Leu Ser Ser  
65 70 75 80  
Ile Leu Tyr Phe Val Gly Ser Leu Val Met Leu Trp Ser Pro Asn Val  
85 90 95  
Tyr Val Leu Leu Leu Gly Arg Leu Leu Asp Gly Phe Gly Val Gly Leu  
100 105 110  
Val Val Thr Leu Val Pro Ile Tyr Ile Ser Glu Thr Ala Pro Pro Glu  
115 120 125  
Ile Arg Gly Leu Leu Asn Thr Leu Pro Gln Phe Thr Gly Ser Gly Gly  
130 135 140  
Met Phe Leu Ser Tyr Cys Met Val Phe Gly Met Ser Leu Met Pro Ser  
145 150 155 160  
Pro Ser Trp Arg Leu Met Leu Gly Val Leu Phe Ile Pro Ser Leu Val  
165 170 175  
Phe Phe Phe Leu Thr Val Phe Phe Leu Pro Glu Ser Pro Arg Trp Leu  
180 185 190  
Val Ser Lys Gly Arg Met Leu Glu Ala Lys Arg Val Leu Gln Arg Leu  
195 200 205  
Arg Gly Arg Glu Asp Val Ser Gly Glu Met Ala Leu Leu Val Glu Gly  
210 215 220  
Leu Gly Ile Gly Gly Glu Thr Thr Ile Glu Glu Tyr Ile Ile Gly Pro  
225 230 235 240  
Ala Asp Glu Val Thr Asp Asp His Asp Ile Ala Val Asp Lys Asp Gln  
245 250 255  
Ile Lys Leu Tyr Gly Ala Glu Glu Gly Leu Ser Trp Val Ala Arg Pro  
260 265 270

BB-1163 US DIV Correct Sequence Listing

val Lys Gly Gly Ser Thr Met Ser Val Leu Ser Arg His Gly Ser Thr  
 275 280 285  
 Met Ser Arg Arg Gln Gly Ser Leu Ile Asp Pro Leu Val Thr Leu Phe  
 290 295 300  
 Gly Ser Val His Glu Lys Met Pro Asp Thr Gly Ser Met Arg Ser Ala  
 305 310 315 320  
 Leu Phe Pro His Phe Gly Ser Met Phe Ser Val Gly Gly Asn Gln Pro  
 325 330 335  
 Arg His Glu Asp Trp Asp Glu Glu Asn Leu Val Gly Glu Gly Glu Asp  
 340 345 350  
 Tyr Pro Ser Asp His Gly Asp Asp Ser Glu Asp Asp Leu His Ser Pro  
 355 360 365  
 Leu Ile Ser Arg Gln Thr Thr Ser Met Glu Lys Asp Met Pro His Thr  
 370 375 380  
 Ala His Gly Thr Leu Ser Thr Phe Arg His Gly Ser Gln Val Gln Gly  
 385 390 395 400  
 Ala Gln Gly Glu Gly Ala Gly Ser Met Gly Ile Gly Gly Trp Gln  
 405 410 415  
 val Ala Trp Lys Trp Thr Glu Arg Glu Asp Glu Ser Gly Gln Lys Glu  
 420 425 430  
 Glu Gly Phe Pro Gly Ser Arg Arg Gly Ser Ile Val Ser Leu Pro Gly  
 435 440 445  
 Gly Asp Gly Thr Gly Glu Ala Asp Phe Val Gln Ala Ser Ala Leu Val  
 450 455 460  
 Ser Gln Pro Ala Leu Tyr Ser Lys Asp Leu Leu Lys Glu His Thr Ile  
 465 470 475 480  
 Gly Pro Ala Met Val His Pro Ser Glu Thr Thr Lys Gly Ser Ile Trp  
 485 490 495  
 His Asp Leu His Asp Pro Gly Val Lys Arg Ala Leu Val Val Gly Val  
 500 505 510  
 Gly Leu Gln Ile Leu Gln Gln Phe Ser Gly Ile Asn Gly Val Leu Tyr  
 515 520 525  
 Tyr Thr Pro Gln Ile Leu Glu Gln Ala Gly Val Gly Ile Leu Leu Ser  
 530 535 540  
 Asn Met Gly Ile Ser Ser Ser Ala Ser Leu Leu Ile Ser Ala Leu  
 545 550 555 560  
 Thr Thr Phe Val Met Leu Pro Ala Ile Ala Val Ala Met Arg Leu Met  
 565 570 575  
 Asp Leu Ser Gly Arg Arg Thr Leu Leu Leu Thr Thr Ile Pro Ile Leu  
 580 585 590  
 Ile Ala Ser Leu Leu Val Leu Val Ile Ser Asn Leu Val His Met Asn  
 595 600 605

BB-1163 US DIV Correct Sequence Listing

Ser Ile val His Ala val Leu Ser Thr Val Ser Val Val Leu Tyr Phe  
610 615 620  
Cys Phe Phe Val Met Gly Phe Gly Pro Ala Pro Asn Ile Leu Cys Ser  
625 630 635 640  
Glu Ile Phe Pro Thr Arg Val Arg Gly Ile Cys Ile Ala Ile Cys Ala  
645 650 655  
Leu Thr Phe Trp Ile Cys Asp Ile Ile Val Thr Tyr Ser Leu Pro Val  
660 665 670  
Leu Leu Lys Ser Ile Gly Leu Ala Gly Val Phe Gly Met Tyr Ala Ile  
675 680 685  
Val Cys Cys Ile Ser Trp Val Phe Val Phe Ile Lys Val Pro Glu Thr  
690 695 700  
Lys Gly Met Pro Leu Glu Val Ile Thr Glu Phe Phe Ser Val Gly Ala  
705 710 715 720  
Arg Gln Ala Glu Ala Ala Lys Asn Glu  
725

<210> 30

<211> 549

<212> PRT

<213> Beta vulgaris

<400> 30  
Met Ser Glu Gly Thr Asn Lys Ala Met Ser Asp Pro Pro Pro Thr Thr  
1 5 10 15  
Ala Ser Lys Val Ile Ala Asp Phe Asp Pro Leu Lys Lys Pro Pro Lys  
20 25 30  
Arg Asn Lys Phe Ala Phe Ala Cys Ala Thr Leu Ala Ser Met Thr Ser  
35 40 45  
Val Leu Leu Gly Tyr Asp Ile Gly Val Met Ser Gly Ala Ile Ile Tyr  
50 55 60  
Leu Lys Glu Asp Trp His Ile Ser Asp Thr Gln Ile Gly Val Leu Val  
65 70 75 80  
Gly Ile Leu Asn Ile Tyr Cys Leu Phe Gly Ser Phe Ala Ala Gly Arg  
85 90 95  
Thr Ser Asp Trp Ile Gly Arg Arg Tyr Thr Ile Val Leu Ala Gly Ala  
100 105 110  
Ile Phe Phe Val Gly Ala Leu Leu Met Gly Phe Ala Thr Asn Tyr Ala  
115 120 125  
Phe Leu Met Val Gly Arg Phe Val Thr Gly Ile Gly Val Gly Tyr Ala  
130 135 140  
Leu Met Ile Ala Pro Val Tyr Thr Ala Glu Val Ser Pro Ala Ser Ser  
145 150 155 160  
Arg Gly Phe Leu Thr Ser Phe Pro Glu Val Phe Ile Asn Ala Gly Ile  
165 170 175

BB-1163 US DIV Correct Sequence Listing

Leu Leu Gly Tyr Ile Ser Asn Leu Ala Phe Ser Ser Leu Pro Thr His  
 180 185 190  
 Leu Ser Trp Arg Phe Met Leu Gly Ile Gly Ala Ile Pro Ser Ile Phe  
 195 200 205  
 Leu Ala Ile Gly Val Leu Ala Met Pro Glu Ser Pro Arg Trp Leu Val  
 210 215 220  
 Met Gln Gly Arg Leu Gly Asp Ala Lys Lys Val Leu Asn Arg Ile Ser  
 225 230 235 240  
 Asp Ser Pro Glu Glu Ala Gln Leu Arg Leu Ser Glu Ile Lys Gln Thr  
 245 250 255  
 Ala Gly Ile Pro Ala Glu Cys Asp Glu Asp Ile Tyr Lys Val Glu Lys  
 260 265 270  
 Thr Lys Ile Lys Ser Gly Asn Ala Val Trp Lys Glu Leu Phe Phe Asn  
 275 280 285  
 Pro Thr Pro Ala Val Arg Arg Ala Val Ile Ala Gly Ile Gly Ile His  
 290 295 300  
 Phe Phe Gln Gln Ala Ser Gly Ile Asp Ala Val Val Leu Tyr Ser Pro  
 305 310 315 320  
 Arg Ile Phe Gln Ser Ala Gly Ile Thr Asn Ala Arg Lys Gln Leu Leu  
 325 330 335  
 Ala Thr Val Ala Val Gly Val Val Lys Thr Leu Phe Ile Leu Val Ala  
 340 345 350  
 Thr Phe Gln Leu Asp Lys Tyr Gly Arg Arg Pro Leu Leu Leu Thr Ser  
 355 360 365  
 Val Gly Gly Met Ile Ile Ala Ile Leu Thr Leu Ala Met Ser Leu Thr  
 370 375 380  
 Val Ile Asp His Ser His His Lys Ile Thr Trp Ala Ile Ala Leu Cys  
 385 390 395 400  
 Ile Thr Met Val Cys Ala Val Val Ala Ser Phe Ser Ile Gly Leu Gly  
 405 410 415  
 Pro Ile Thr Trp Val Tyr Ser Ser Glu Val Phe Pro Leu Arg Leu Arg  
 420 425 430  
 Ala Gln Gly Thr Ser Met Gly Val Ala Val Asn Arg Val Val Ser Gly  
 435 440 445  
 Val Ile Ser Ile Phe Phe Leu Pro Leu Ser His Lys Ile Thr Thr Gly  
 450 455 460  
 Gly Ala Phe Phe Leu Phe Gly Gly Ile Ala Ile Ile Ala Trp Phe Phe  
 465 470 475 480  
 Phe Leu Thr Phe Leu Pro Glu Thr Arg Gly Arg Thr Leu Glu Asn Met  
 485 490 495  
 His Glu Leu Phe Glu Asp Phe Arg Trp Arg Glu Ser Phe Pro Gly Asn  
 500 505 510

BB-1163 US DIV Correct Sequence Listing

Lys Ser Asn Asn Asp Glu Asn Ser Thr Arg Lys Gln Ser Asn Gly Asn  
515 520 525

Asp Lys Ser Gln Val Gln Leu Gly Glu Thr Thr Ser Thr Thr Val  
530 535 540

Thr Asn Asp Asn His  
545